

SEQUENCE LISTING

<110> Jegla, Timothy James
ICAgen, Inc.

<120> Kv10.1, a Novel Voltage-Gated Potassium Channel From
Human Brain

<130> 018512-005910US

<140> US 09/833,466

<141> 2001-04-11

<150> US 60/197,793

<151> 2000-04-14

<160> 18

<170> PatentIn Ver. 2.1

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<213> Homo sapiens

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channel Kv10.1

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<222> (151)..(1788)

<223> Kv10.1

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aac acg acg gag aat gag ggc agc caa cac cgc agg agc att tgc tcc 96
Asn Thr Thr Glu Asn Glu Gly Ser Gln His Arg Arg Ser Ile Cys Ser
 20 25 30

ctg ggt gcc cgt tcc ggc tcc cag gcc agc atc cac ggc tgg aca gag 144
Leu Gly Ala Arg Ser Gly Ser Gln Ala Ser Ile His Gly Trp Thr Glu
 35 40 45

ggc aac tat aac tac tac atc gag gaa gac gaa gac ggg gag gag gag 192
Gly Asn Tyr Asn Tyr Tyr Ile Glu Glu Asp Glu Asp Gly Glu Glu Glu
 50 55 60

gac cag tgg aag gac gac ctg gca gaa gag gac cag cag gca ggg gag 240
Asp Gln Trp Lys Asp Asp Leu Ala Glu Glu Asp Gln Gln Ala Gly Glu
 65 70 75 80

gtc acc acc gcc aag ccc gag ggc ccc agc gac cct ccg gcc ctg ctg 288
Val Thr Thr Ala Lys Pro Glu Gly Pro Ser Asp Pro Pro Ala Leu Leu
 85 90 95

tcc acg ctg aat gtg aac gtg ggt ggc cac agc tac cag ctg gac tac 336
Ser Thr Leu Asn Val Asn Val Gly Gly His Ser Tyr Gln Leu Asp Tyr
100 105 110

tgc gag ctg gcc ggc ttc ccc aag acg cgc cta ggt cgc ctg gcc acc 384
Cys Glu Leu Ala Gly Phe Pro Lys Thr Arg Leu Gly Arg Leu Ala Thr
115 120 125

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tcc acc agc cgc agc cgc cag cta agc ctg tgc gac gac tac gag gag Ser Thr Ser Arg Ser Arg Gln Leu Ser Leu Cys Asp Asp Tyr Glu Glu 130 135 140	432
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gtc tac aat ttc tac ctg tcc ggg gtg ctg ctg gtg ctc gac ggg ctg Val Tyr Asn Phe Tyr Leu Ser Gly Val Leu Leu Val Leu Asp Gly Leu 165 170 175	528
tgt ccg cgc cgc ttc ctg gag gag ctg ggc tac tgg ggc gtg cgg ctc Cys Pro Arg Arg Phe Leu Glu Glu Leu Gly Tyr Trp Gly Val Arg Leu 180 185 190	576
aag tac acg cca cgc tgc tgc cgc atc tgc ttc gag gag cgg cgc gac Lys Tyr Thr Pro Arg Cys Cys Arg Ile Cys Phe Glu Glu Arg Arg Asp 195 200 205	624
gag ctg agc gaa cgg ctc aag atc cag cac gag ctg cgc gcg cag gcg Glu Leu Ser Glu Arg Leu Lys Ile Gln His Glu Leu Arg Ala Gln Ala 210 215 220	672
cag gtc gag gag gcg gag gaa ctc ttc cgc gac atg cgc ttc tac ggc Gln Val Glu Glu Ala Glu Glu Leu Phe Arg Asp Met Arg Phe Tyr Gly 225 230 235 240	720
ccg cag cgg cgc cgc ctc tgg aac ctc atg gag aag cca ttc tcc tcg Pro Gln Arg Arg Leu Trp Asn Leu Met Glu Lys Pro Phe Ser Ser 245 250 255	768
gtg gcc gcc aag gcc atc ggg gtg gcg tcc agc acc ttc gtg ctc gtc Val Ala Ala Lys Ala Ile Gly Val Ala Ser Ser Thr Phe Val Leu Val 260 265 270	816
tcc gtg gtg gcg ctg gcg ctc aac acc gtg gag gag atg cag cag cac Ser Val Val Ala Leu Ala Leu Asn Thr Val Glu Glu Met Gln Gln His 275 280 285	864
tcg ggg cag ggc gag ggc ggc cca gac ctg cgg ccc atc ctg gag cac Ser Gly Gln Gly Glu Gly Gly Pro Asp Leu Arg Pro Ile Leu Glu His 290 295 300	912
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cta gcc tcc acg ccc gac ctg agg cgc ttc gcg cgc agc gcc ctc aac Leu Ala Ser Thr Pro Asp Leu Arg Arg Phe Ala Arg Ser Ala Leu Asn 325 330 335	1008
ctg gtg gac ctg gtg gcc atc ctg ccg ctc tac ctt cag ctg ctg ctc Leu Val Asp Leu Val Ala Ile Leu Pro Leu Tyr Leu Gln Leu Leu Leu 340 345 350	1056
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Val Gly Lys Val Gly Gln Val Leu Arg Val Met Arg Leu Met Arg Ile	
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Phe Arg Ile Leu Lys Leu Ala Arg His Ser Thr Gly Leu Arg Ala Phe	
385 390 395 400	
ggc ttc acg ctg cgc cag tgc tac cag cag gtg ggc tgc ctg ctg ctc	1248
Gly Phe Thr Leu Arg Gln Cys Tyr Gln Val Gly Cys Leu Leu Leu	
405 410 415	
ttc atc gcc atg ggc atc ttc act ttc tct gcg gct gtc tac tct gtg	1296
Phe Ile Ala Met Gly Ile Phe Thr Phe Ser Ala Ala Val Tyr Ser Val	
420 425 430	
gag cac gat gtg ccc agc acc aac ttc act acc atc ccc cac tcc tgg	1344
Glu His Asp Val Pro Ser Thr Asn Phe Thr Thr Ile Pro His Ser Trp	
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tgg tgg gcc gcg gtg agc atc tcc acc gtg ggc tac gga gac atg tac	1392
Trp Trp Ala Ala Val Ser Ile Ser Thr Val Gly Tyr Gly Asp Met Tyr	
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cca gag acc cac ctg ggc agg ttt ttt gcc ttc ctc tgc att gct ttt	1440
Pro Glu Thr His Leu Gly Arg Phe Phe Ala Phe Leu Cys Ile Ala Phe	
465 470 475 480	
ggg atc att ctc aac ggg atg ccc att tcc atc ctc tac aac aag ttt	1488
Gly Ile Ile Leu Asn Gly Met Pro Ile Ser Ile Leu Tyr Asn Lys Phe	
485 490 495	
tct gat tac tac agc aag ctg aag gct tat gag tat acc acc ata cgc	1536
Ser Asp Tyr Tyr Ser Lys Leu Lys Ala Tyr Glu Tyr Thr Thr Ile Arg	
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agg gag agg gga gag gtg aac ttc atg cag aga gcc aga aag aag ata	1584
Arg Glu Arg Gly Glu Val Asn Phe Met Gln Arg Ala Arg Lys Lys Ile	
515 520 525	
gct gag tgt ttg ctt gga agc aac cca cag ctc acc cca aga caa gag	1632
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channel Kv10.1	
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channel Kv10.1	

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Leu	Gly	Ala	Arg	Ser	Gly	Ser	Gln	Ala	Ser	Ile	His	Gly	Trp	Thr	Glu
		35					40					45			
Gly	Asn	Tyr	Asn	Tyr	Tyr	Ile	Glu	Glu	Asp	Glu	Asp	Gly	Glu	Glu	Glu
	50					55					60				
Asp	Gln	Trp	Lys	Asp	Asp	Leu	Ala	Glu	Glu	Asp	Gln	Gln	Ala	Gly	Glu
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Val	Thr	Thr	Ala	Lys	Pro	Glu	Gly	Pro	Ser	Asp	Pro	Pro	Ala	Leu	Leu
				85					90					95	
Ser	Thr	Leu	Asn	Val	Asn	Val	Gly	Gly	His	Ser	Tyr	Gln	Leu	Asp	Tyr
			100					105					110		
Cys	Glu	Leu	Ala	Gly	Phe	Pro	Lys	Thr	Arg	Leu	Gly	Arg	Leu	Ala	Thr
		115					120					125			
Ser	Thr	Ser	Arg	Ser	Arg	Gln	Leu	Ser	Leu	Cys	Asp	Asp	Tyr	Glu	Glu
		130				135					140				
Gln	Thr	Asp	Glu	Tyr	Phe	Phe	Asp	Arg	Asp	Pro	Ala	Val	Phe	Gln	Leu
145				150						155					160
Val	Tyr	Asn	Phe	Tyr	Leu	Ser	Gly	Val	Leu	Leu	Val	Leu	Asp	Gly	Leu
			165						170					175	
Cys	Pro	Arg	Arg	Phe	Leu	Glu	Glu	Leu	Gly	Tyr	Trp	Gly	Val	Arg	Leu
			180					185					190		
Lys	Tyr	Thr	Pro	Arg	Cys	Cys	Arg	Ile	Cys	Phe	Glu	Glu	Arg	Arg	Asp
		195					200					205			
Glu	Leu	Ser	Glu	Arg	Leu	Lys	Ile	Gln	His	Glu	Leu	Arg	Ala	Gln	Ala
	210					215					220				
Gln	Val	Glu	Glu	Ala	Glu	Glu	Leu	Phe	Arg	Asp	Met	Arg	Phe	Tyr	Gly
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Pro	Gln	Arg	Arg	Arg	Leu	Trp	Asn	Leu	Met	Glu	Lys	Pro	Phe	Ser	Ser
			245						250					255	
Val	Ala	Ala	Lys	Ala	Ile	Gly	Val	Ala	Ser	Ser	Thr	Phe	Val	Leu	Val
			260					265					270		
Ser	Val	Val	Ala	Leu	Ala	Leu	Asn	Thr	Val	Glu	Glu	Met	Gln	Gln	His
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Ser	Gly	Gln	Gly	Glu	Gly	Gly	Pro	Asp	Leu	Arg	Pro	Ile	Leu	Glu	His
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Val	Glu	Met	Leu	Cys	Met	Gly	Phe	Phe	Thr	Leu	Glu	Tyr	Leu	Leu	Arg
305				310						315					320
Leu	Ala	Ser	Thr	Pro	Asp	Leu	Arg	Arg	Phe	Ala	Arg	Ser	Ala	Leu	Asn
			325						330					335	
Leu	Val	Asp	Leu	Val	Ala	Ile	Leu	Pro	Leu	Tyr	Leu	Gln	Leu	Leu	Leu
			340					345					350		
Glu	Cys	Phe	Thr	Gly											

Gly Ile Ile Leu Asn Gly Met Pro Ile Ser Ile Leu Tyr Asn Lys Phe
 485 490 495
 Ser Asp Tyr Tyr Ser Lys Leu Lys Ala Tyr Glu Tyr Thr Thr Ile Arg
 500 505 510
 Arg Glu Arg Gly Glu Val Asn Phe Met Gln Arg Ala Arg Lys Lys Ile
 515 520 525
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 Asn
 545

<210> 4
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:sense Oligo 1

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<210> 5
 <211> 24
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 <213> Artificial Sequence

<220>
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<400> 5
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<210> 6
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
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 gene-specific antisense Oligo 3

<400> 6
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<210> 7
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 <212> DNA
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<400> 7
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<210> 8
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 <220>
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 <212> DNA
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 <212> DNA
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 <223> Description of Artificial Sequence:antisense Oligo
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 <400> 10
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 <210> 11
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 <220>
 <223> Description of Artificial Sequence:coding region
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			20					25					30		
Val	Gly	Gly	Leu	Ala	His	Glu	Val	Leu	Trp	Arg	Thr	Leu	Asp	Arg	Leu
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Pro	Arg	Thr	Arg	Leu	Gly	Lys	Leu	Arg	Asp	Cys	Asn	Thr	His	Asp	Ser
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Leu	Leu	Glu	Val	Cys	Asp	Tyr	Ser	Leu	Asp	Asp	Asn	Glu	Tyr	Phe	
65					70				75					80	
Phe	Asp	Arg	His	Pro	Gly	Ala	Phe	Thr	Ser	Ile	Leu	Asn	Phe	Tyr	Arg
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Thr	Gly	Arg	Leu	His	Met	Met	Glu	Glu	Met	Cys	Ala	Leu	Ser	Phe	Ser
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Gln	Glu	Leu	Asp	Tyr	Trp	Gly	Ile	Asp	Glu	Ile	Tyr	Leu	Glu	Ser	Cys
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Asn	Thr	Cys	Cys	Ala	Glu	Lys	Arg	Lys	Lys	Leu	Trp	Asp	Leu	Leu	Glu
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Lys	Pro	Asn	Ser	Ser	Val	Ala	Ala	Lys	Ile	Leu	Ala	Ile	Ile	Ser	Ile
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Met	Phe	Ile	Val	Leu	Ser	Thr	Ile	Ala	Leu	Ser	Leu	Asn	Thr	Leu	Pro
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225					230				235					240	
Leu	Leu	Arg	Phe	Leu	Ser	Ser	Pro	Lys	Lys	Trp	Lys	Phe	Phe	Lys	Gly
			245					250					255		
Pro	Leu	Asn	Ala	Ile	Asp	Leu	Leu	Ala	Ile	Leu	Pro	Tyr	Tyr	Val	Thr
		260						265					270		
Ile	Phe	Leu	Thr	Glu	Ser	Asn	Lys	Ser	Val	Leu	Gln	Phe	Gln	Asn	Val
	275					280						285			
Arg	Arg	Val	Val	Gln	Ile	Phe	Arg	Ile	Met	Arg	Ile	Leu	Arg	Ile	Leu
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Gly	Ile	Met	Ile	Phe	Ser	Ser	Leu	Val	Phe	Phe	Ala	Glu	Lys	Asp	Glu
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Asp	Asp	Thr	Lys	Phe	Lys	Ser	Ile	Pro	Ala	Ser	Phe	Trp	Trp	Ala	Thr
	355					360						365			
Ile	Thr	Met	Thr	Thr	Val	Gly	Tyr	Gly	Asp	Ile	Tyr	Pro	Lys	Thr	Leu
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Ile	Ala	Leu	Pro	Ile	Pro	Ile	Ile	Val	Asn	Asn	Phe	Ser	Glu	Phe	Tyr
			405						410				415		
Lys	Glu	Gln	Lys	Arg	Gln	Glu	Lys	Ala	Ile	Lys	Arg	Arg	Glu	Ala	Leu
		420					425					430			
Glu	Arg	Ala	Lys	Arg	Asn	Gly	Ser	Ile	Val	Ser	Met	Asn	Met	Lys	Asp
	435					440					445				
Ala	Phe	Ala	Arg	Ser	Ile	Glu	Met	Met	Asp	Ile	Val	Val	Glu	Lys	Asn
	450					455					460				
Gly	Glu	Asn	Met	Gly	Lys	Lys	Asp	Lys	Val	Gln	Asp	Asn	His	Leu	Ser
465					470				475					480	

Pro Asn Lys Trp Lys Trp Thr Lys Arg Thr Leu Ser Glu Thr Ser Ser
 485 490 495
 Ser Lys Ser Phe Glu Thr Lys Glu Gln Gly Ser Pro Glu Lys Ala Arg
 500 505 510
 Ser Ser Ser Ser Pro Gln His Leu Asn Val Gln Gln Leu Glu Asp Met
 515 520 525
 Tyr Asn Lys Met Ala Lys Thr Gln Ser Gln Pro Ile Leu Asn Thr Lys
 530 535 540
 Glu Ser Ala Ala Gln Ser Lys Pro Lys Glu Glu Leu Glu Met Glu Ser
 545 550 555 560
 Ile Pro Ser Pro Val Ala Pro Leu Pro Thr Arg Thr Glu Gly Val Ile
 565 570 575
 Asp Met Arg Ser Met Ser Ser Ile Asp Ser Phe Ile Ser Cys Ala Thr
 580 585 590
 Asp Phe Pro Glu Ala Thr Arg Phe Ser His Ser Pro Leu Thr Ser Leu
 595 600 605
 Pro Ser Lys Thr Gly Gly Ser Thr Ala Pro Glu Val Gly Trp Arg Gly
 610 615 620
 Ala Leu Gly Ala Ser Gly Gly Arg Phe Val Glu Ala Asn Pro Ser Pro
 625 630 635 640
 Asp Ala Ser Gln His Ser Ser Phe Phe Ile Glu Ser Pro Lys Ser Ser
 645 650 655
 Met Lys Thr Asn Asn Pro Leu Lys Leu Arg Ala Leu Lys Val Asn Phe
 660 665 670
 Met Glu Gly Asp Pro Ser Pro Leu Leu Pro Val Leu Gly Met Tyr His
 675 680 685
 Asp Pro Leu Arg Asn Arg Gly Ser Ala Ala Ala Val Ala Gly Leu
 690 695 700
 Glu Cys Ala Thr Leu Leu Asp Lys Ala Val Leu Ser Pro Glu Ser Ser
 705 710 715 720
 Ile Tyr Thr Thr Ala Ser Ala Lys Thr Pro Pro Arg Ser Pro Glu Lys
 725 730 735
 His Thr Ala Ile Ala Phe Asn Phe Glu Ala Gly Val His Gln Tyr Ile
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 Asp Ala Asp Thr Asp Asp Glu Gly Gln Leu Leu Tyr Ser Val Asp Ser
 755 760 765
 Ser Pro Pro Lys Ser Leu Pro Gly Ser Thr Ser Pro Lys Phe Ser Thr
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 Gly Thr Arg Ser Glu Lys Asn His Phe Glu Ser Ser Pro Leu Pro Thr
 785 790 795 800
 Ser Pro Lys Phe Leu Arg Gln Asn Cys Ile Tyr Ser Thr Glu Ala Leu
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 Thr Gly Lys Gly Pro Ser Gly Gln Glu Lys Cys Lys Leu Glu Asn His
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<223> human voltage-gated potassium channel Kv2.2

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Cys	Ser	Arg	Arg	Val	Lys	Ile	Asn	Val	Gly	Gly	Leu	Asn	His	Glu	Val	35	40	45
Leu	Trp	Arg	Thr	Leu	Asp	Arg	Leu	Pro	Arg	Thr	Arg	Leu	Gly	Lys	Leu	50	55	60
Arg	Asp	Cys	Asn	Thr	His	Glu	Ser	Leu	Leu	Glu	Val	Cys	Asp	Asp	Tyr	65	70	75
Asn	Leu	Asn	Glu	Asn	Glu	Tyr	Phe	Phe	Asp	Arg	His	Pro	Gly	Ala	Phe	85	90	95
Thr	Ser	Ile	Leu	Asn	Phe	Tyr	Arg	Thr	Gly	Lys	Leu	His	Met	Met	Glu	100	105	110
Glu	Met	Cys	Ala	Leu	Ser	Phe	Gly	Gln	Glu	Leu	Asp	Tyr	Trp	Gly	Ile	115	120	125
Asp	Glu	Ile	Tyr	Leu	Glu	Ser	Cys	Cys	Gln	Ala	Arg	Tyr	His	Gln	Lys	130	135	140
Lys	Glu	Gln	Met	Asn	Glu	Glu	Leu	Arg	Arg	Glu	Ala	Glu	Thr	Met	Arg	145	150	155
Asp	Gly	Glu	Gly	Glu	Phe	Asp	Asn	Thr	Cys	Cys	Pro	Asp	Lys	Arg		165	170	175
Lys	Lys	Leu	Trp	Asp	Leu	Leu	Glu	Lys	Pro	Asn	Ser	Ser	Val	Ala	Ala	180	185	190
Lys	Ile	Leu	Ala	Ile	Val	Ser	Ile	Leu	Phe	Ile	Val	Leu	Ser	Thr	Ile	195	200	205
Ala	Leu	Ser	Leu	Asn	Thr	Leu	Pro	Glu	Leu	Gln	Glu	Thr	Asp	Glu	Phe	210	215	220
Gly	Gln	Leu	Asn	Asp	Asn	Arg	Gln	Leu	Ala	His	Val	Glu	Ala	Val	Cys	225	230	235
Ile	Ala	Trp	Phe	Thr	Met	Glu	Tyr	Leu	Leu	Arg	Phe	Leu	Ser	Ser	Pro	245	250	255
Asn	Lys	Trp	Lys	Phe	Phe	Lys	Gly	Pro	Leu	Asn	Val	Ile	Asp	Leu	Leu	260	265	270
Ala	Ile	Leu	Pro	Tyr	Tyr	Val	Thr	Ile	Phe	Leu	Thr	Glu	Ser	Asn	Lys	275	280	285
Ser	Val	Leu	Gln	Phe	Gln	Asn	Val	Arg	Arg	Val	Val	Gln	Ile	Phe	Arg	290	295	300
Ile	Met	Arg	Ile	Leu	Arg	Ile	Leu	Lys	Leu	Ala	Arg	His	Ser	Thr	Gly	305	310	315
Leu	Gln	Ser	Leu	Gly	Phe	Thr	Leu	Arg	Arg	Ser	Tyr	Asn	Glu	Leu	Gly	325	330	335
Leu	Leu	Ile	Leu	Phe	Leu	Ala	Met	Gly	Ile	Met	Ile	Phe	Ser	Ser	Leu	340	345	350
Val	Phe	Phe	Ala	Glu	Lys	Asp	Glu	Asp	Ala	Thr	Lys	Phe	Thr	Ser	Ile	355	360	365
Pro	Ala	Ser	Phe	Trp	Trp	Ala	Thr	Ile	Thr	Met	Thr	Thr	Val	Gly	Tyr	370	375	380
Gly	Asp	Ile	Tyr	Pro	Lys	Thr	Leu	Leu	Gly	Lys	Ile	Val	Gly	Gly	Leu	385	390	395
Cys	Cys	Ile	Ala	Gly	Val	Leu	Val	Ile	Ala	Leu	Pro	Ile	Pro	Ile	Ile	405	410	415
Val	Asn	Asn	Phe	Ser	Glu	Phe	Tyr	Lys	Glu	Gln	Lys	Arg	Gln	Glu	Lys	420	425	430
Ala	Ile	Lys	Arg	Arg	Glu	Ala	Leu	Glu	Arg	Ala	Lys	Arg	Asn	Gly	Ser	435	440	445
Ile	Val	Ser	Met	Asn	Leu	Lys	Asp	Ala	Phe	Ala	Arg	Ser	Met	Glu	Leu	450	455	460
Ile	Asp	Val	Ala	Val	Glu	Lys	Ala	Gly	Glu	Ser	Ala	Asn	Thr	Lys	Asp	465	470	475
Ser	Ala	Asp	Asp	Asn	His	Leu	Ser	Pro	Ser	Arg	Trp	Lys	Trp	Ala	Arg	485	490	495

Lys Ala Leu Ser Glu Thr Ser Ser Asn Lys Ser Phe Glu Asn Lys Tyr
 500 505 510
 Gln Glu Val Ser Gln Lys Asp Ser His Glu Gln Leu Asn Asn Thr Phe
 515 520 525
 Ser Ser Ser Pro Gln His Leu Ser Ala Gln Lys Leu Glu Met Leu Tyr
 530 535 540
 Asn Glu Ile Thr Lys Thr Gln Pro His Ser His Pro Asn Pro Asp Cys
 545 550 555 560
 Gln Glu Lys Pro Glu Arg Pro Ser Ala Tyr Glu Glu Glu Ile Glu Met
 565 570 575
 Glu Glu Val Val Cys Pro Gln Glu Gln Leu Ala Val Ala Gln Thr Glu
 580 585 590
 Val Ile Val Asp Met Lys Ser Thr Ser Ser Ile Asp Ser Phe Thr Ser
 595 600 605
 Cys Ala Thr Asp Phe Thr Glu Thr Glu Arg Ser Pro Leu Pro Pro Pro
 610 615 620
 Ser Ala Ser His Leu Gln Met Lys Phe Pro Thr Asp Leu Pro Gly Thr
 625 630 635 640
 Glu Glu His Gln Arg Ala Arg Gly Pro Pro Phe Leu Thr Leu Ser Arg
 645 650 655
 Glu Lys Gly Pro Ala Ala Arg Asp Gly Thr Leu Glu Tyr Ala Pro Val
 660 665 670
 Asp Ile Thr Val Asn Leu Asp Ala Ser Gly Ser Gln Cys Gly Leu His
 675 680 685
 Ser Pro Leu Gln Ser Asp Asn Ala Thr Asp Ser Pro Lys Ser Ser Leu
 690 695 700
 Lys Gly Ser Asn Pro Leu Lys Ser Arg Ser Leu Lys Val Asn Phe Lys
 705 710 715 720
 Glu Asn Arg Gly Ser Ala Pro Gln Thr Pro Pro Ser Thr Ala Arg Pro
 725 730 735
 Leu Pro Val Thr Thr Ala Asp Phe Ser Leu Thr Thr Pro Gln His Ile
 740 745 750
 Ser Thr Ile Leu Leu Glu Glu Thr Pro Ser Gln Gly Asp Arg Pro Cys
 755 760 765
 Trp Ala Leu Arg Phe Gln Arg Leu Val Arg Asp Leu Pro Lys Gly Cys
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 Pro Pro Gly Phe Pro Ser Arg Asn Cys Ser Leu Ser Leu Gln Glu Arg
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 Gly Gly Ala Ser Leu Lys
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<212> PRT

<213> Homo sapiens

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<223> S6 domain of voltage-gated potassium channel
Kv10.1

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Pro Ile Ser Ile Leu Tyr Asn Lys Phe Ser
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amplification primer

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amplification primer

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